

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: BASF Aktiengesellschaft
- (B) STREET:
- (C) CITY: Ludwigshafen
- (E) COUNTRY: Deutschland
- (F) POSTAL CODE (ZIP): 67065

(ii) TITLE OF INVENTION: Neue Poly ADP Ribose Polymerase Gene

(iii) NUMBER OF SEQUENCES: 28

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC DOS/MS DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

## (vi) ORIGINAL SOURCE:

- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1715
- (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

|   |    |
|---|----|
| CC ATG GCG GCG CGG CGG CGA CGG AGC ACC GGC GGC GGC AGG GCG AGA  | 47 |
| Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg     |    |
| 1 5 10 15   |    |
|   |    |
| GCA TTA AAT GAA AGC AAA AGA GTT AAT AAT GGC AAC ACG GCT CCA GAA | 95 |
| Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| GAC TCT TCC CCT GCC AAG AAA ACT CGT AGA TGC CAG AGA CAG GAG TCG<br>Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser<br>35 40 45        | 143 |
| AAA AAG ATG CCT GTG GCT GGA GGA AAA GCT AAT AAG GAC AGG ACA GAA<br>Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu<br>50 55 60        | 191 |
| GAC AAG CAA GAT GAA TCT GTG AAG GCC TTG CTG TTA AAG GGC AAA GCT<br>Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala<br>65 70 75        | 239 |
| CCT GTG GAC CCA GAG TGT ACA GCC AAG GTG GGG AAG GCT CAT GTG TAT<br>Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr<br>80 85 90 95     | 287 |
| TGT GAA GGA AAT GAT GTC TAT GAT GTC ATG CTA AAT CAG ACC AAT CTC<br>Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu<br>100 105 110     | 335 |
| CAG TTC AAC AAC AAC AAG TAC TAT CTG ATT CAG CTA TTA GAA GAT GAT<br>Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp<br>115 120 125     | 383 |
| GCC CAG AGG AAC TTC AGT GTT TGG ATG AGA TGG GGC CGA GTT GGG AAA<br>Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys<br>130 135 140     | 431 |
| ATG GGA CAG CAC AGC CTG GTG GCT TGT TCA GGC AAT CTC AAC AAG GCC<br>Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala<br>145 150 155     | 479 |
| AAG GAA ATC TTT CAG AAG AAA TTC CTT GAC AAA ACG AAA AAC AAT TGG<br>Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp<br>160 165 170 175 | 527 |
| GAA GAT CGA GAA AAG TTT GAG AAG GTG CCT GGA AAA TAT GAT ATG CTA<br>Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu<br>180 185 190     | 575 |
| CAG ATG GAC TAT GCC ACC AAT ACT CAG GAT GAA GAG GAA ACA AAG AAA<br>Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Thr Lys Lys<br>195 200 205         | 623 |
| GAG GAA TCT CTT AAA TCT CCC TTG AAG CCA GAG TCA CAG CTA GAT CTT<br>Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu<br>210 215 220     | 671 |
| CGG GTA CAG GAG TTA ATA AAG TTG ATC TGT AAT GTT CAG GCC ATG GAA<br>Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu<br>225 230 235     | 719 |
| GAA ATG ATG ATG GAA ATG AAG TAT AAT ACC AAG AAA GCC CCA CTT GGG<br>Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly<br>240 245 250 255 | 767 |
| AAG CTG ACA GTG GCA CAA ATC AAG GCA GGT TAC CAG TCT CTT AAG AAG<br>Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys                    | 815 |

|  | 260 | 265 | 270 |      |
|--|-----|-----|-----|------|
| ATT GAG GAT TGT ATT CGG GCT GGC CAG CAT GGA CGA GCT CTC ATG GAA<br>Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu | 275 | 280 | 285 | 863  |
| GCA TGC AAT GAA TTC TAC ACC AGG ATT CCG CAT GAC TTT GGA CTC CGT<br>Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg | 290 | 295 | 300 | 911  |
| ACT CCT CCA CTA ATC CGG ACA CAG AAG GAA CTG TCA GAA AAA ATA CAA<br>Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln | 305 | 310 | 315 | 959  |
| TTA CTA GAG GCT TTG GGA GAC ATT GAA ATT GCT ATT AAG CTG GTG AAA<br>Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys | 320 | 325 | 330 | 1007 |
| ACA GAG CTA CAA AGC CCA GAA CAC CCA TTG GAC CAA CAC TAT AGA AAC<br>Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn | 340 | 345 | 350 | 1055 |
| CTA CAT TGT GCC TTG CGC CCC CTT GAC CAT GAA AGT TAC GAG TTC AAA<br>Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys | 355 | 360 | 365 | 1103 |
| GTG ATT TCC CAG TAC CTA CAA TCT ACC CAT GCT CCC ACA CAC AGC GAC<br>Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp | 370 | 375 | 380 | 1151 |
| TAT ACC ATG ACC TTG CTG GAT TTG TTT GAA GTG GAG AAG GAT GGT GAG<br>Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu | 385 | 390 | 395 | 1199 |
| AAA GAA GCC TTC AGA GAG GAC CTT CAT AAC AGG ATG CTT CTA TGG CAT<br>Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His | 400 | 405 | 410 | 1247 |
| GGT TCC AGG ATG AGT AAC TGG GTG GGA ATC TTG AGC CAT GGG CTT CGA<br>Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg | 420 | 425 | 430 | 1295 |
| ATT GCC CCA CCT GAA GCT CCC ATC ACA GGT TAC ATG TTT GGG AAA GGA<br>Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly | 435 | 440 | 445 | 1343 |
| ATC TAC TTT GCT GAC ATG TCT TCC AAG AGT GCC AAT TAC TGC TTT GCC<br>Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala | 450 | 455 | 460 | 1391 |
| TCT CGC CTA AAG AAT ACA GGA CTG CTG CTC TTA TCA GAG GTA GCT CTA<br>Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Ser Glu Val Ala Leu     | 465 | 470 | 475 | 1439 |
| GGT CAG TGT AAT GAA CTA CTA GAG GCC AAT CCT AAG GCC GAA GGA TTG<br>Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu | 480 | 485 | 490 | 495  |
| CTT CAA GGT AAA CAT AGC ACC AAG GGG CTG GGC AAG ATG GCT CCC AGT  |     |     |     | 1487 |
|  |     |     |     | 1535 |

|  |     |      |
|--|-----|------|
| Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser    |     |      |
| 500  | 505 | 510  |
| TCT GCC CAC TTC GTC ACC CTG AAT GGG AGT ACA GTG CCA TTA GGA CCA    |     | 1583 |
| Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro    |     |      |
| 515  | 520 | 525  |
| GCA AGT GAC ACA GGA ATT CTG AAT CCA GAT GGT TAT ACC CTC AAC TAC    |     | 1631 |
| Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr    |     |      |
| 530  | 535 | 540  |
| AAT GAA TAT ATT GTA TAT AAC CCC AAC CAG GTC CGT ATG CGG TAC CTT    |     | 1679 |
| Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu    |     |      |
| 545  | 550 | 555  |
| TTA AAG GTT CAG TTT AAT TTC CTT CAG CTG TGG TGA ATGTTGATAT         |     | 1725 |
| Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp *                      |     |      |
| 560  | 565 | 570  |
| TAAATAAACCG AGAGATCTGA TCTTCAAGCA AGAAAATAAG CAGTGGTGTA CTTGTGAATT |     | 1785 |
| TTGTGATATT TTATGTAATA AAAACTGTAC AGGTCTAAAAA AAAAAAAA AAAAAAAA     |     | 1843 |

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

|   |     |     |    |
|---|-----|-----|----|
| Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala |     |     |    |
| 1   | 5   | 10  | 15 |
| Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp |     |     |    |
| 20  | 25  | 30  |    |
| Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys |     |     |    |
| 35  | 40  | 45  |    |
| Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp |     |     |    |
| 50  | 55  | 60  |    |
| Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala Pro     |     |     |    |
| 65  | 70  | 75  | 80 |
| Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys |     |     |    |
| 85  | 90  | 95  |    |
| Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln |     |     |    |
| 100   | 105 | 110 |    |
| Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala |     |     |    |
| 115   | 120 | 125 |    |
| Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met |     |     |    |

130

135

140

Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys  
 145 150 155 160

Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu  
 165 170 175

Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln  
 180 185 190

Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu  
 195 200 205

Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg  
 210 215 220

Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu  
 225 230 235 240

Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys  
 245 250 255

Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile  
 260 265 270

Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala  
 275 280 285

Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr  
 290 295 300

Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu  
 305 310 315 320

Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr  
 325 330 335

Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu  
 340 345 350

His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val  
 355 360 365

Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr  
 370 375 380

Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys  
 385 390 395 400

Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly  
 405 410 415

Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile  
 420 425 430

Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile  
 435 440 445

Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser

450

455

460

Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly  
 465 470 475 480

Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu  
 485 490 495

Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser  
 500 505 510

Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala  
 515 520 525

Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn  
 530 535 540

Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu  
 545 550 555 560

Lys Val Gln Phe Asn Phe Leu Gln Leu Trp \*  
 565 570

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 242..1843
- (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

|  |     |
|--|-----|
| TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA  | 60  |
| TAGCCGATGT CTAATCCCCC ACACAAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC   | 120 |
| TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG  | 180 |
| GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATGTCCCTGC TTTTCTTGGC  | 240 |
| C ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT GAG<br>Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu | 286 |

| 575   | 580 | 585 |      |
|---|-----|-----|------|
| AAG AAG AAG GGC CGG CAG GCA GGA AGG GAG GAG GAC CCC TTC CGC TCC<br>Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser<br>590 | 595 | 600 | 334  |
| ACC GCT GAG GCC CTC AAG GCC ATA CCC GCA GAG AAG CGC ATA ATC CGC<br>Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg<br>605 | 610 | 615 | 382  |
| GTG GAT CCA ACA TGT CCA CTC AGC AGC AAC CCC GGG ACC CAG GTG TAT<br>Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr<br>620 | 625 | 630 | 430  |
| GAG GAC TAC AAC TGC ACC CTG AAC CAG ACC AAC ATC GAG AAC AAC AAC<br>Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn<br>635 | 640 | 645 | 478  |
| AAC AAG TTC TAC ATC ATC CAG CTG CTC CAA GAC AGC AAC CGC TTC TTC<br>Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe<br>655 | 660 | 665 | 526  |
| ACC TGC TGG AAC CGC TGG GGC CGT GTG GGA GAG GTC GGC CAG TCA AAG<br>Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys<br>670 | 675 | 680 | 574  |
| ATC AAC CAC TTC ACA AGG CTA GAA GAT GCA AAG AAG GAC TTT GAG AAG<br>Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys<br>685 | 690 | 695 | 622  |
| AAA TTT CGG GAA AAG ACC AAG AAC AAC TGG GCA GAG CGG GAC CAC TTT<br>Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe<br>700 | 705 | 710 | 670  |
| GTG TCT CAC CCG GGC AAG TAC ACA CTT ATC GAA GTA CAG GCA GAG GAT<br>Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp<br>715 | 720 | 725 | 718  |
| GAG GCC CAG GAA GCT GTG GTG AAG GTG GAC AGA GGC CCA GTG AGG ACT<br>Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr<br>735 | 740 | 745 | 766  |
| GTG ACT AAG CGG GTG CAG CCC TGC TCC CTG GAC CCA GCC ACG CAG AAG<br>Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys<br>750 | 755 | 760 | 814  |
| CTC ATC ACT AAC ATC TTC AGC AAG GAG ATG TTC AAG AAC ACC ATG GCC<br>Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala<br>765 | 770 | 775 | 862  |
| CTC ATG GAC CTG GAT GTG AAG AAG ATG CCC CTG GGA AAG CTG AGC AAG<br>Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys<br>780 | 785 | 790 | 910  |
| CAA CAG ATT GCA CGG GGT TTC GAG GCC TTG GAG GCG CTG GAG GAG GCC<br>Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Ala<br>795     | 800 | 805 | 958  |
| CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC TCA   |     |     | 1006 |

|   |      |      |      |
|---|------|------|------|
| Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser |      |      |      |
| 815   | 820  | 825  |      |
| CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC CCG |      | 1054 |      |
| His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro |      |      |      |
| 830   | 835  | 840  |      |
| CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG CTG |      | 1102 |      |
| Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu |      |      |      |
| 845   | 850  | 855  |      |
| GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT GAG |      | 1150 |      |
| Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu |      |      |      |
| 860   | 865  | 870  |      |
| CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC TAC |      | 1198 |      |
| Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr |      |      |      |
| 875   | 880  | 885  | 890  |
| CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT GAG |      | 1246 |      |
| Gln Leu Leu Lys Cys Gln Leu Gln Leu Asp Ser Gly Ala Pro Glu     |      |      |      |
| 895   | 900  | 905  |      |
| TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC AGG |      | 1294 |      |
| Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg |      |      |      |
| 910   | 915  | 920  |      |
| TGC CCT ACA CTT CAA CAC ATC TGG AAA GTA AAC CAA GAA GGG GAG GAA |      | 1342 |      |
| Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu |      |      |      |
| 925   | 930  | 935  |      |
| GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG TGG |      | 1390 |      |
| Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp |      |      |      |
| 940   | 945  | 950  |      |
| CAT GGC ACC AAC ATG GCC GTG GTG GCC GCC ATC CTC ACT AGT GGG CTC |      | 1438 |      |
| His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu |      |      |      |
| 955   | 960  | 965  | 970  |
| CGC ATC ATG CCA CAT TCT GGT GGG CGT GTT GGC AAG GGC ATC TAC TTT |      | 1486 |      |
| Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe |      |      |      |
| 975   | 980  | 985  |      |
| GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG TGT |      | 1534 |      |
| Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys |      |      |      |
| 990   | 995  | 1000 |      |
| GGG GCC CAC CAT GTC TAC ATG TTC CTG GGT GAG GTG GCC CTG GGC     |      | 1582 |      |
| Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly |      |      |      |
| 1005  | 1010 | 1015 |      |
| AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA CCT |      | 1630 |      |
| Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro |      |      |      |
| 1020  | 1025 | 1030 |      |
| CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT CCG |      | 1678 |      |
| Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro |      |      |      |
| 1035  | 1040 | 1045 | 1050 |

|  |      |
|--|------|
| ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG CCC  | 1726 |
| Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro  |      |
| 1055 1060 1065   |      |
| CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC TCC  | 1774 |
| Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser  |      |
| 1070 1075 1080   |      |
| CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC TAC  | 1822 |
| Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr  |      |
| 1085 1090 1095   |      |
| CTG CTG GAG GTC CAC CTC TGA GTGCCGCC TGTCCTCCGG GGTCTGCAA        | 1873 |
| Leu Leu Glu Val His Leu *  |      |
| 1100 1105  |      |
| GGCTGGACTG TGATCTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTT  | 1933 |
| TTTCAAGAAT ACAATACGTT GTTGTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA | 1993 |
| CTTATGCCTC CTAAC TGAAA TTTGTATTC TTTGACACAT CTGCCAGTC CCTCTCCTCC | 2053 |
| CAGCCCATGG TAACCAGCAT TTGACTCTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC | 2113 |
| ACATGTAAGT GAGATCATGC AGTGTGGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT | 2173 |
| AATGTGCACC GGGTTCACCC ATGTTTCAT AAATGACAAG ATTCCTCCT TTAAAAAAA   | 2233 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                              | 2265 |

## (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

|   |  |
|---|--|
| Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys |  |
| 1 5 10 15   |  |
| Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr |  |
| 20 25 30  |  |
| Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val |  |
| 35 40 45  |  |
| Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu |  |
| 50 55 60  |  |
| Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn |  |
| 65 70 75 80   |  |
| Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr |  |
| 85 90 95  |  |
| Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile |  |

| 100   | 105 | 110 |     |
|---|-----|-----|-----|
| Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys |     |     |     |
| 115   | 120 | 125 |     |
| Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val |     |     |     |
| 130   | 135 | 140 |     |
| Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu |     |     |     |
| 145   | 150 | 155 | 160 |
| Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val |     |     |     |
| 165   | 170 | 175 |     |
| Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu |     |     |     |
| 180   | 185 | 190 |     |
| Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu |     |     |     |
| 195   | 200 | 205 |     |
| Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln |     |     |     |
| 210   | 215 | 220 |     |
| Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Ala Leu     |     |     |     |
| 225   | 230 | 235 | 240 |
| Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His |     |     |     |
| 245   | 250 | 255 |     |
| Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro |     |     |     |
| 260   | 265 | 270 |     |
| Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val |     |     |     |
| 275   | 280 | 285 |     |
| Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln |     |     |     |
| 290   | 295 | 300 |     |
| Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln |     |     |     |
| 305   | 310 | 315 | 320 |
| Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr |     |     |     |
| 325   | 330 | 335 |     |
| Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys |     |     |     |
| 340   | 345 | 350 |     |
| Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Asp     |     |     |     |
| 355   | 360 | 365 |     |
| Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His |     |     |     |
| 370   | 375 | 380 |     |
| Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg |     |     |     |
| 385   | 390 | 395 | 400 |
| Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala |     |     |     |
| 405   | 410 | 415 |     |
| Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly |     |     |     |

|   |     |     |
|---|-----|-----|
| 420   | 425 | 430 |
| Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg |     |     |
| 435   | 440 | 445 |
| Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro |     |     |
| 450   | 455 | 460 |
| Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr |     |     |
| 465   | 470 | 475 |
| Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln |     |     |
| 485   | 490 | 495 |
| Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln |     |     |
| 500   | 505 | 510 |
| Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu |     |     |
| 515   | 520 | 525 |
| Leu Glu Val His Leu *   |     |     |
| 530   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2265 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (F) TISSUE TYPE: Uterus
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 221..1843
  - (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

|   |     |
|---|-----|
| TGGGACTGGT CGCCTGACTC GGCCTGCCCT AGCCTCTGCT TCACCCCACT GGTGGCCAAA | 60  |
| TAGCCGATGT CTAATCCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC | 120 |
| TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG | 180 |
| GGGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATG TCC CTG CTT TTC   | 235 |
| Met Ser Leu Leu Phe   |     |
| 535   |     |
| TTG GCC ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT   | 283 |

|   |     |  |
|---|-----|--|
| Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro |     |  |
| 540 545 550 555   |     |  |
| GAG AAG AAG AAG GGC CGG CAG GCA GGA AGG GAG GAC CCC TTC CGC     | 331 |  |
| Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg |     |  |
| 560 565 570   |     |  |
| TCC ACC GCT GAG GCC CTC AAG GCC ATA CCC GCA GAG AAG CGC ATA ATC | 379 |  |
| Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile |     |  |
| 575 580 585   |     |  |
| CGC GTG GAT CCA ACA TGT CCA CTC AGC AGC AAC CCC GGG ACC CAG GTG | 427 |  |
| Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val |     |  |
| 590 595 600   |     |  |
| TAT GAG GAC TAC AAC TGC ACC CTG AAC CAG ACC AAC ATC GAG AAC AAC | 475 |  |
| Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn |     |  |
| 605 610 615   |     |  |
| AAC AAC AAG TTC TAC ATC ATC CAG CTG CTC CAA GAC AGC AAC CGC TTC | 523 |  |
| Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe |     |  |
| 620 625 630 635   |     |  |
| TTC ACC TGC TGG AAC CGC TGG GGC CGT GTG GGA GAG GTC GGC CAG TCA | 571 |  |
| Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser |     |  |
| 640 645 650   |     |  |
| AAG ATC AAC CAC TTC ACA AGG CTA GAA GAT GCA AAG AAG GAC TTT GAG | 619 |  |
| Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu |     |  |
| 655 660 665   |     |  |
| AAG AAA TTT CGG GAA AAG ACC AAG AAC AAC TGG GCA GAG CGG GAC CAC | 667 |  |
| Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His |     |  |
| 670 675 680   |     |  |
| TTT GTG TCT CAC CCG GGC AAG TAC ACA CTT ATC GAA GTA CAG GCA GAG | 715 |  |
| Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu |     |  |
| 685 690 695   |     |  |
| GAT GAG GCC CAG GAA GCT GTG GTG AAG GTG GAC AGA GGC CCA GTG AGG | 763 |  |
| Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg |     |  |
| 700 705 710 715   |     |  |
| ACT GTG ACT AAG CGG GTG CAG CCC TGC TCC CTG GAC CCA GCC ACG CAG | 811 |  |
| Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln |     |  |
| 720 725 730   |     |  |
| AAG CTC ATC ACT AAC ATC TTC AGC AAG GAG ATG TTC AAG AAC ACC ATG | 859 |  |
| Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met |     |  |
| 735 740 745   |     |  |
| GCC CTC ATG GAC CTG GAT GTG AAG AAG ATG CCC CTG GGA AAG CTG AGC | 907 |  |
| Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser |     |  |
| 750 755 760   |     |  |
| AAG CAA CAG ATT GCA CGG GGT TTC GAG GCC TTG GAG GCG CTG GAG GAG | 955 |  |
| Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu |     |  |
| 765 770 775   |     |  |

|   |      |
|---|------|
| GCC CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC | 1003 |
| Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser |      |
| 780 785 790 795   |      |
| TCA CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC | 1051 |
| Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro |      |
| 800 805 810   |      |
| CCG CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG | 1099 |
| Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu |      |
| 815 820 825   |      |
| CTG GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT | 1147 |
| Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser |      |
| 830 835 840   |      |
| GAG CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC | 1195 |
| Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp |      |
| 845 850 855   |      |
| TAC CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT | 1243 |
| Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro |      |
| 860 865 870 875   |      |
| GAG TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC | 1291 |
| Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His |      |
| 880 885 890   |      |
| AGG TGC CCT ACA CTT CAA CAC ATC TGG AAA GTA AAC CAA GAA GGG GAG | 1339 |
| Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu |      |
| 895 900 905   |      |
| GAA GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG | 1387 |
| Glu Asp Arg Phe Gln Ala His Ser Lys Leu Glu Asn Arg Lys Leu Leu |      |
| 910 915 920   |      |
| TGG CAT GGC ACC AAC ATG GCC GTG GTG GCC GCC ATC CTC ACT AGT GGG | 1435 |
| Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly |      |
| 925 930 935   |      |
| CTC CGC ATC ATG CCA CAT TCT GGT GGG CGT GTT GGC AAG GGC ATC TAC | 1483 |
| Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr |      |
| 940 945 950 955   |      |
| TTT GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG | 1531 |
| Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys |      |
| 960 965 970   |      |
| TGT GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG | 1579 |
| Cys Gly Ala His His Val Gly Tyr Met Phe Leu Glu Val Ala Leu     |      |
| 975 980 985   |      |
| GGC AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA | 1627 |
| Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro |      |
| 990 995 1000  |      |
| CCT CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT | 1675 |
| Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp |      |

1005

1010

1015

|  |      |
|--|------|
| CCG ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG    | 1723 |
| Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val    |      |
| 1020 1025 1030 1035  |      |
| CCC CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC    | 1771 |
| Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe    |      |
| 1040 1045 1050   |      |
| TCC CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC    | 1819 |
| Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg    |      |
| 1055 1060 1065   |      |
| TAC CTG CTG GAG GTC CAC CTC TGA GTGCCGCCCGG TGTCCCCGGG GGTCCCTGCAA | 1873 |
| Tyr Leu Leu Glu Val His Leu *                                      |      |
| 1070 1075  |      |
| GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT  | 1933 |
| TTTCAAGAAT ACAATACGTT GTTGTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA   | 1993 |
| CTTATGCCTC CTAAC TGAAA TTTGTATTC TTTGACACAT CTGCCAGTC CCTCTCCTCC   | 2053 |
| CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC  | 2113 |
| ACATGTAACT GAGATCATGC AGTGTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT    | 2173 |
| AATGTGCACC GGGTTCACCC ATGTTTCAT AAATGACAAG ATTCCTCCT TTAAAAAAA     | 2233 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                                | 2265 |

## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

|   |  |
|---|--|
| Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val |  |
| 1 5 10 15   |  |
| Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu |  |
| 20 25 30  |  |
| Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala |  |
| 35 40 45  |  |
| Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn |  |
| 50 55 60  |  |
| Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr |  |
| 65 70 75 80   |  |
| Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln     |  |

85

90

95

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly  
 100 105 110

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala  
 115 120 125

Lys Lys Asp Phe Glu Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp  
 130 135 140

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile  
 145 150 155 160

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp  
 165 170 175

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu  
 180 185 190

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met  
 195 200 205

Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro  
 210 215 220

Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu  
 225 230 235 240

Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser  
 245 250 255

Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe  
 260 265 270

Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala  
 275 280 285

Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala  
 290 295 300

Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His  
 305 310 315 320

Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu  
 325 330 335

Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln  
 340 345 350

Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val  
 355 360 365

Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly  
 370 375 380

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala  
 385 390 395 400

Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val

405

410

415

Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr  
 420 425 430

Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu  
 435 440 445

Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro  
 450 455 460

Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly  
 465 470 475 480

His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly  
 485 490 495

Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe  
 500 505 510

Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser  
 515 520 525

Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu \*  
 530 535 540

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 112..1710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCGGGCTTTC ACTTTTCTG CTGCCTCGGG GAACACCTCG AGCCAACTGC TTCCTAACTC 60

AGGGTGGGCA GAACTGACGG GATCTAAGCT TCTGCATCTC TGAGGAGAAC C ATG GCT 117  
 Met Ala

CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG CAG CGA 165  
 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg  
 545 550 555

|   |     |
|---|-----|
| CAA GGG ACA GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG GCT CTC<br>Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu<br>560 565 570 575         | 213 |
| AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC TCA TGT<br>Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys<br>580 585 590     | 261 |
| CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT GAC TGT<br>Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys<br>595 600 605     | 309 |
| ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAG TTC TAT ATT<br>Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe Tyr Ile<br>610 615 620             | 357 |
| ATC CAA CTG CTG GAG GGT AGT CGC TTC TTC TGC TGG AAT CGC TGG<br>Ile Gln Leu Leu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp<br>625 630 635             | 405 |
| GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC ACC TGC<br>Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys<br>640 645 650 655 | 453 |
| CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG AAG ACT<br>Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu Lys Thr<br>660 665 670         | 501 |
| AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC AAC AAG<br>Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys<br>675 680 685     | 549 |
| TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG GCT GTA<br>Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val<br>690 695 700     | 597 |
| GTG AAG GCC TTA TCT CCC CAG GTG GAC AGC GGC CCT GTG AGG ACC GTG<br>Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val<br>705 710 715     | 645 |
| GTC AAG CCC TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC<br>Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn<br>720 725 730 735 | 693 |
| ATC TTC AGC AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG<br>Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu<br>740 745 750     | 741 |
| GAT GTG AAG AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC<br>Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala<br>755 760 765     | 789 |
| CGT GGC TTC GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC<br>Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Ala Met Lys Asn Pro<br>770 775 780         | 837 |
| ACA GGG GAT GGC CAG AGC CTG GAA GAG CTC TCC TGC TTC TAC ACT<br>Thr Gly Asp Gly Gln Ser Leu Glu Leu Ser Ser Cys Phe Tyr Thr                            | 885 |

| 785   | 790  | 795  |      |
|---|------|------|------|
| GTC ATC CCA CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC |      |      | 933  |
| Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser |      |      |      |
| 800   | 805  | 810  | 815  |
| CCT GAT GTG CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC |      |      | 981  |
| Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp |      |      |      |
| 820   | 825  | 830  |      |
| ATC GAG TTG GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG |      |      | 1029 |
| Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu     |      |      |      |
| 835   | 840  | 845  |      |
| AAA GTG GAA GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC |      |      | 1077 |
| Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu |      |      |      |
| 850   | 855  | 860  |      |
| AGG TGC CAG CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA |      |      | 1125 |
| Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala |      |      |      |
| 865   | 870  | 875  |      |
| ATA CAG ACC TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC |      |      | 1173 |
| Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn |      |      |      |
| 880   | 885  | 890  | 895  |
| CTG CGG CAT GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC |      |      | 1221 |
| Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe |      |      |      |
| 900   | 905  | 910  |      |
| CAG GCC CAC TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC |      |      | 1269 |
| Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr |      |      |      |
| 915   | 920  | 925  |      |
| AAT GTG GCC GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG |      |      | 1317 |
| Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met |      |      |      |
| 930   | 935  | 940  |      |
| CCA CAC TCG GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG     |      |      | 1365 |
| Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu |      |      |      |
| 945   | 950  | 955  |      |
| AAC AGC AAG TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC |      |      | 1413 |
| Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly His     |      |      |      |
| 960   | 965  | 970  | 975  |
| CAG GTG GGC TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC |      |      | 1461 |
| Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His |      |      |      |
| 980   | 985  | 990  |      |
| CAC ATC ACC ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT |      |      | 1509 |
| His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe |      |      |      |
| 995   | 1000 | 1005 |      |
| GAC AGC GTC ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC |      |      | 1557 |
| Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp |      |      |      |
| 1010  | 1015 | 1020 |      |
| ATT GAA CTT GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG |      |      | 1605 |

|   |      |      |      |
|---|------|------|------|
| Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro |      |      |      |
| 1025  | 1030 | 1035 |      |
| CCT GTG CAG TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA |      |      | 1653 |
| Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Phe Ser Gln Ser Glu     |      |      |      |
| 1040  | 1045 | 1050 | 1055 |
| TAC CTC ATA TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG |      |      | 1701 |
| Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Glu     |      |      |      |
| 1060  | 1065 | 1070 |      |
| ATT CAC CTC TAAGCTGCTT GCCCTCCCTA GGTCCAAGCC                    |      |      | 1740 |
| Ile His Leu   |      |      |      |

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

|   |     |     |     |
|---|-----|-----|-----|
| Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys |     |     |     |
| 1   | 5   | 10  | 15  |
| Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu |     |     |     |
| 20  | 25  | 30  |     |
| Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro |     |     |     |
| 35  | 40  | 45  |     |
| Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr |     |     |     |
| 50  | 55  | 60  |     |
| Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe |     |     |     |
| 65  | 70  | 75  | 80  |
| Tyr Ile Ile Gln Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn     |     |     |     |
| 85  | 90  | 95  |     |
| Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe |     |     |     |
| 100   | 105 | 110 |     |
| Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu     |     |     |     |
| 115   | 120 | 125 |     |
| Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro |     |     |     |
| 130   | 135 | 140 |     |
| Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu |     |     |     |
| 145   | 150 | 155 | 160 |
| Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg |     |     |     |
| 165   | 170 | 175 |     |
| Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile |     |     |     |

| 180   | 185 | 190 |
|---|-----|-----|
| Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met |     |     |
| 195   | 200 | 205 |
| Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln |     |     |
| 210   | 215 | 220 |
| Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys |     |     |
| 225   | 230 | 235 |
| Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe |     |     |
| 245   | 250 | 255 |
| Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile |     |     |
| 260   | 265 | 270 |
| Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu |     |     |
| 275   | 280 | 285 |
| Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu |     |     |
| 290   | 295 | 300 |
| Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln |     |     |
| 305   | 310 | 315 |
| Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr |     |     |
| 325   | 330 | 335 |
| Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys |     |     |
| 340   | 345 | 350 |
| Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp |     |     |
| 355   | 360 | 365 |
| Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His |     |     |
| 370   | 375 | 380 |
| Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg |     |     |
| 385   | 390 | 395 |
| Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala |     |     |
| 405   | 410 | 415 |
| Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly |     |     |
| 420   | 425 | 430 |
| Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys |     |     |
| 435   | 440 | 445 |
| Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro |     |     |
| 450   | 455 | 460 |
| Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala |     |     |
| 465   | 470 | 475 |
| Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln |     |     |
| 485   | 490 | 495 |
| Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln |     |     |

500

505

510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu  
 515 520 525

Leu Glu Ile His Leu  
 530

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mus musculus*

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1584

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

|   |     |
|---|-----|
| ATG GCT CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG | 48  |
| Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys |     |
| 535 540 545   |     |
| CAG CGA CAA GGG ACA GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG     | 96  |
| Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu     |     |
| 550 555 560 565   |     |
| GCT CTC AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC | 144 |
| Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro |     |
| 570 575 580   |     |
| TCA TGT CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT | 192 |
| Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr |     |
| 585 590 595   |     |
| GAC TGT ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAG TTC     | 240 |
| Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe     |     |
| 600 605 610   |     |
| TAT ATT ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT | 288 |
| Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn |     |
| 615 620 625   |     |
| CGC TGG GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC | 336 |
| Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe |     |
| 630 635 640 645   |     |

|   |      |
|---|------|
| ACC TGC CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG | 384  |
| Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu     |      |
| 650 655 660   |      |
| AAG ACT AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC | 432  |
| Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro |      |
| 665 670 675   |      |
| AAC AAG TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG | 480  |
| Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu |      |
| 680 685 690   |      |
| GCT GTA GTG AAG GTG GAC AGC GGC CCT GTG AGG ACC GTG GTC AAG CCC | 528  |
| Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro |      |
| 695 700 705   |      |
| TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC ATC TTC AGC | 576  |
| Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser |      |
| 710 715 720 725   |      |
| AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG GAT GTG AAG | 624  |
| Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys |      |
| 730 735 740   |      |
| AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC CGT GGC TTC | 672  |
| Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe |      |
| 745 750 755   |      |
| GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC ACA GGG GAT | 720  |
| Glu Ala Leu Glu Ala Leu Glu Ala Met Lys Asn Pro Thr Gly Asp     |      |
| 760 765 770   |      |
| GGC CAG AGC CTG GAA GAG CTC TCC TGC TTC TAC ACT GTC ATC CCA     | 768  |
| Gly Gln Ser Leu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro     |      |
| 775 780 785   |      |
| CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC CCT GAT GTG | 816  |
| His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val |      |
| 790 795 800 805   |      |
| CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC ATC GAG TTG | 864  |
| Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu |      |
| 810 815 820   |      |
| GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG AAA GTG GAA | 912  |
| Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu     |      |
| 825 830 835   |      |
| GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC AGG TGC CAG | 960  |
| Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln |      |
| 840 845 850   |      |
| CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA ATA CAG ACC | 1008 |
| Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr |      |
| 855 860 865   |      |
| TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC CTG CGG CAT | 1056 |
| Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His |      |

| 870   | 875  | 880  | 885  |      |
|---|------|------|------|------|
| GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC CAG GCC CAC |      |      |      | 1104 |
| Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His |      |      |      |      |
| 890   | 895  | 900  |      |      |
| TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC AAT GTG GCC |      |      |      | 1152 |
| Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala |      |      |      |      |
| 905   | 910  | 915  |      |      |
| GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG CCA CAC TCG |      |      |      | 1200 |
| Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser |      |      |      |      |
| 920   | 925  | 930  |      |      |
| GGT GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG AAC AGC AAG |      |      |      | 1248 |
| Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys |      |      |      |      |
| 935   | 940  | 945  |      |      |
| TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC CAG GTG GGC |      |      |      | 1296 |
| Ser Ala Gly Tyr Val Thr Met His Cys Gly Gly His Gln Val Gly     |      |      |      |      |
| 950   | 955  | 960  | 965  |      |
| TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC CAC ATC ACC |      |      |      | 1344 |
| Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr |      |      |      |      |
| 970   | 975  | 980  |      |      |
| ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT GAC AGC GTC |      |      |      | 1392 |
| Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val |      |      |      |      |
| 985   | 990  | 995  |      |      |
| ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC ATT GAA CTT |      |      |      | 1440 |
| Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu |      |      |      |      |
| 1000  | 1005 | 1010 |      |      |
| GAA CTG GAT GGG CAG CCG GTG GTG CCC CAA GGC CCG CCT GTG CAG     |      |      |      | 1488 |
| Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln |      |      |      |      |
| 1015  | 1020 | 1025 |      |      |
| TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA TAC CTC ATA |      |      |      | 1536 |
| Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile |      |      |      |      |
| 1030  | 1035 | 1040 | 1045 |      |
| TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG ATT CAC CTC |      |      |      | 1584 |
| Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu |      |      |      |      |
| 1050  | 1055 | 1060 |      |      |
| TAA   |      |      |      | 1587 |

## (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 528 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys

1

5

10

15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe  
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe  
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu  
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro  
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu  
 145 150 155 160

Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro  
 165 170 175

Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser  
 180 185 190

Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys  
 195 200 205

Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe  
 210 215 220

Glu Ala Leu Glu Ala Leu Glu Ala Met Lys Asn Pro Thr Gly Asp  
 225 230 235 240

Gly Gln Ser Leu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro  
 245 250 255

His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val  
 260 265 270

Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu  
 275 280 285

Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu  
 290 295 300

Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln  
 305 310 315 320

Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr

| 325   | 330                             | 335 |     |
|---|---------------------------------|-----|-----|
| Tyr Leu Lys Gln Thr Gly Asn Ser                                 | Tyr Arg Cys Pro Asn Leu Arg His |     |     |
| 340   | 345                             | 350 |     |
| Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His |                                 |     |     |
| 355   | 360                             | 365 |     |
| Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala |                                 |     |     |
| 370   | 375                             | 380 |     |
| Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser |                                 |     |     |
| 385   | 390                             | 395 | 400 |
| Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys |                                 |     |     |
| 405   | 410                             | 415 |     |
| Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly |                                 |     |     |
| 420   | 425                             | 430 |     |
| Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr |                                 |     |     |
| 435   | 440                             | 445 |     |
| Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val |                                 |     |     |
| 450   | 455                             | 460 |     |
| Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu |                                 |     |     |
| 465   | 470                             | 475 | 480 |
| Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln |                                 |     |     |
| 485   | 490                             | 495 |     |
| Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile |                                 |     |     |
| 500   | 505                             | 510 |     |
| Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu |                                 |     |     |
| 515   | 520                             | 525 |     |

## (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 2
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5  
andere Aminosaeuren"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (iii) HYPOTHETICAL: YES

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

## (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:10
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys  
1 5 10 15  
Gly Ile Tyr Phe Ala  
20

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:16
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:21
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:24
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:25
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa  
1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly  
20 25 30

Ile Tyr Phe Ala Xaa Xaa Ser Lys Ser Ala Xaa Tyr  
35 40 45

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Leu oder Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |     |     | 15  |     |
| Xaa |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 20  |     |

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:21
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Asp oder Glu"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:22
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 10 oder 11 andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Xaa |
| 1   |     |     |     |     |     |     |     |     |     | 5   |     |     |     |     | 10  |     |     | 15  |     |
| Gln | Leu | Leu | Xaa | Xaa | Xaa | Trp | Gly | Arg | Val | Gly |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Xaa | Xaa | Xaa | Phe | Xaa | Lys | Xaa | Xaa | Xaa | Xaa | Lys | Thr | Xaa | Asn | Xaa |
| 1   |     |     |     | 5   |     |     |     |     |     |     |     | 10  |     |     | 15  |
| Trp | Xaa | Xaa | Xaa | Xaa | Xaa | Phe | Xaa | Xaa | Xaa | Pro | Xaa | Lys |     |     |     |
|     |     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 44 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

(A) NAME/KEY: Region  
(B) LOCATION: 4  
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder  
Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Xaa | Leu | Xaa | Xaa | Xaa | Ile | Xaa |
| 1   |     |     |     |     |     | 5   |     |     |     |     |     |     | 10  |     | 15  |
| Met | Xaa | Pro | Leu | Gly | Lys | Leu |
|     |     |     |     |     |     | 20  |     |     |     |     | 25  |     | 30  |     |     |
| Xaa | Xaa | Xaa | Gln | Ile | Xaa | Leu |
|     |     |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa  
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

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- (A) NAME/KEY: Region
- (B) LOCATION:14
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 7 bis 9  
andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly             | Xaa | Xaa | Ser | Xaa | Xaa | Xaa | Xaa | Gly | Xaa | Xaa | Xaa | Pro | Xaa | Leu | Xaa |
| 1               |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly Xaa Xaa Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                 |     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Tyr oder  
Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Xaa | Xaa | Xaa | Tyr | Xaa | Xaa | Xaa | Gln | Xaa | Xaa | Xaa | Tyr | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

|                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met             | Ala | Ala | Arg | Arg | Arg | Arg | Ser | Thr | Gly | Gly | Gly | Arg | Ala | Arg | Ala |
| 1               |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Leu Asn Glu Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

20

## (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Glu | Leu | Gln | Ser | Pro | Glu | His | Pro | Leu | Asp | Gln | His | Tyr | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | His | Cys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Lys | Gly | Arg | Gln | Ala | Gly | Arg | Glu | Glu | Asp | Pro | Phe | Arg | Ser | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Glu | Ala | Leu | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

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Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu  
1 5 10 15  
Glu Ala Leu Lys  
20

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu  
1 5 10 15  
Ala Leu Lys

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu  
1 5 10 15  
Ala Met Lys